

FIGURE 1 (1/2)

	1	50
{CAA69226}	MQIPRAALLP LLLLLLAAPA SAQLSRAGRS APLAAGCPDR CEPARCPPQP	
{PRSS11-Like}	~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~	
{AAB94569}	~~~~~ ~~~~~ ~MAAPRAGRGA GWSLRAWRA LGGIRWGRRP	
Consensus	----- ----- ----- ----- ----- -----	
	51	100
{CAA69226}	EHCEGGRARD ACGCCEVCGA PEGAACGLQE GPCGEGLQCV VPFGVPASAT	
{PRSS11-Like}	~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~	
{AAB94569}	RLTPDLRALL TSGTSD...P RARVTYGTTPS LWARLSVGVT EPRACLTSGT	
Consensus	----- ----- ----- ----- ----- -----	
	101	150
{CAA69226}	VRRRAQAGLC VCASSEPVCG SDANTYANLC QLRAASRRSE RLHRPPVIVL	
{PRSS11-Like}	~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~	
{AAB94569}	PGPRAQLTAV TPPDTRTREAS ENSGTRSRAW LAVALGAGGA VLLLLWGGR	
Consensus	----- ----- ----- ----- ----- -----	
	151	200
{CAA69226}	QRGACGQQQE D..PNSLRHK YNFIADVVEK IAPAVVHIEL FRKLPSKRE	
{PRSS11-Like}	ALPA.SAGLH Q..LSSPRYK FNFIADVVEK IAPAVVHIEL FLRHPLFGRN	
{AAB94569}	GPPAVLAAVP SPPPASPRSQ YNFIADVVEK TAPAVVYIEI LDRHPFLGRE	
Consensus	---A--- ---S-R-- -NFIADVVEK -APAVV-IE- ---P---R-	
	201	250
{CAA69226}	VPVASGSGFI VSEDGLIVTN AHVVTN.... .KHRVKVEL KNGATYEAKI	
{PRSS11-Like}	VPLSSGSGFI MSEAGLIITM AHVVSSNSAA PGRQQLKVQL QNGDSYEATI	
{AAB94569}	VPISNGSGFV VAADGLIVTN AHVVAD.... .RRRVVRVRL LSGDTYEAVV	
Consensus	VP---GSGF- ---GLI-TN AHVV----- V-L --G--YEA--	

FIGURE 1 (1/2)

	251	*	300
{CAA69226}	KDVDEKADIA LIKIDHQGKL PVLLLGRSSE LRPGEFVVAI GSPFSLQNTV		
{PRSS11-Like}	KDIDKKSDIA TIKIHPKKKL PVLLLGHSA D LRPGEFVVAI GSPFALQNTV		
{AAB94569}	TAVDPVADIA TLRIQTKEPL PTLPLGRSAD VRQGEFVVAM GSPFALQNTI		
Consensus	---D---DIA ---I-----L P-L-LG-S-- -R-GEFVVA- GSPF-LQNT-		
	301	*	350
{CAA69226}	TTGIVSTTQR GGKELGLRNS DMDYIQTDAI INYGNNSGGPL VNLDGEVIGI		
{PRSS11-Like}	TTGIVSTAQR EGRELGLRDS DMDYIQTDAI INYGNNSGGPL VNLDGEVIGI		
{AAB94569}	TSGIVSSAQR PARLGLPQT NVEYIQTDAA IDFGNSGGPL VNLDGEVIGV		
Consensus	T-GIVS--QR ----LGL--- ---YIQTDA- I--GNNSGGPL VNLDGEVIG-		
	351		400
{CAA69226}	NTLKVTAGIS FAIPSDKIKK FLTESHDR.Q AKGKAITKKK YIGIRMMSLT		
{PRSS11-Like}	NTLKVTAGIS FAIPSDRITR FLTEFQDK.Q IKD...WKRR FIGIRMRTIT		
{AAB94569}	NTMKVTAGIS FAIPSDRLRE FLHRGEKKNS SSGISGSQRR YIGVMMTLS		
Consensus	NT-KVTAGIS FAIPSD---- FL----- ----- -IG--M----		
	401		450
{CAA69226}	SSKAKELKDR HRDFPDVISG AYIIEVIPDT PAEAGGLKEN DVIIISINGQS		
{PRSS11-Like}	PSLVDELKAS NPDFPEVSSG IYVQEVPNS PSQRGGIQDG DIIVKVNGRP		
{AAB94569}	PSILAELQLR EPSFPDVQHG VLIHKVILGS PAHRAGLRPG DVILAIGEQM		
Consensus	-S---EL--- ---FP-V--G -----V--- P---G--- D-I-----		
	451		489
{CAA69226}	VVSANDVSDV IKRESTLNMV VRRGNEDIMI TVIPEEIDP		
{PRSS11-Like}	LVDSSELQEA VLTESPLLLE VRRGNDDLLF SIAPEVVM~		
{AAB94569}	VQNAEDVYEA VRTQSQLAVQ IRRGRETLTL YVTPEVTE~		
Consensus	-----S-L--- -RRG----- PE-----		

FIGURE 2 (1/1)

HtrA3 (BC034390) x PRSS11-Like (SEO ID No:2):

FIGURE 3 (1/1)

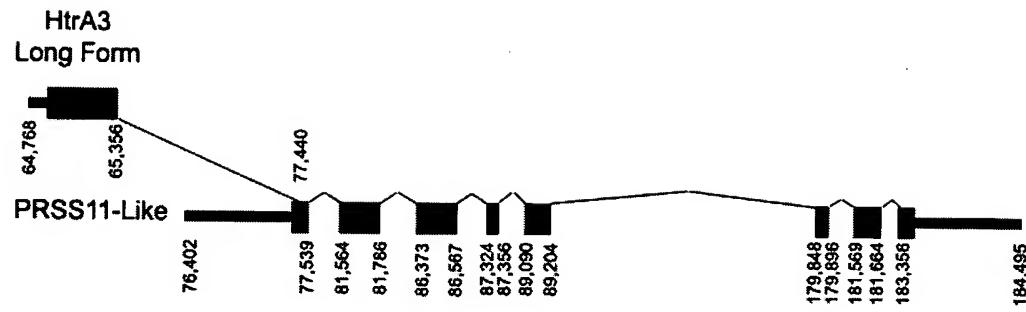


FIGURE 4

A. Unique HtrA3 Long Form Exons

E1 589-bp 12,083-bp E2
GCGCCTGCCCGTTGG~~gta~~agcgctcgggg... ...ttcccgccagcgc~~a~~gGTCTCCACCAGCTGA

E2 100-bp 4,024-bp E3
AGAGCTCTCCTGAG~~gt~~gggtgaatacccc... ...tctccctggctgc~~a~~gACACCCGCTGTTGG

B. Unique PRSS11-Like Exon

E1 1,138-bp 4,024-bp E2
AGAGCTCTCCTGAG~~gt~~gggtgaatacccc... ...tctccctggctgc~~a~~gACACCCGCTGTTGG

C. Common HtrA3 Long form and PRSS11-Like Exons

E3/E2 223-bp 4,586-bp E4/E3
AAGATCCATCCCAAG~~gt~~gggtgggcgtgg... ...ccttctctctcct~~a~~gAAAAAGCTCCCTGTG

E4/E3 195-bp 756-bp E5/E4
GATGCCATCATCAAC~~gt~~gagtcccaggac... ...ttcctcccttg~~c~~agTACGGAACTCCGGG

E5/E4 33-bp 1,733-bp E6/E5
CCACTGGTGAACCTG~~gta~~agtgtcccctag... ...tacccctgccc~~a~~gGATGGCGAGGTCATT

E6/E5 115-bp 90,643-bp E7/E6
ACAAGCAGATCAAAG~~gt~~aaagagactcacct... ...gtgtttcatttcc~~a~~gACTGGAAGAACGCCT

E7/E6 49-bp 1,672-bp E8/E7
GACGATCACACCAAG~~gt~~gagtgtctgaaga... ...gcagactcttcc~~a~~gCCTGGTGGATGAGCT

E8/E7 96-bp 1,691-bp E9/E8 1140-bp
TTCACCTTCTCAGAG~~gt~~aggctctgccaga... ...ctctcctgttgg~~c~~agAGGCAGGCATCCAAGA